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Maximum DB
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Perfect score:
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                                                                                                                                                                                         Post-processing: Minimum Match 0% Maximum Match 100%
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seq
A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
7: geneseqp2001bs:*
                                                                                                                                                                                                                                       length: 0
length: 2000000000
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1198
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Gapop 10.0 ,
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Copyright (c) 1993 - 2004 Compugen Ltd.
geneseqp2002s:*
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                                                                                                                                                                                                                                                                                                                          seqs, 282547505 residues
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1198.211 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	ហ	4	ω	2	ם	Result No.
83	83	83	83	83	83.5	83.5	84	84	84.5	86.5	87.5	89		89		89	90	92	113	113	138.5	1198	1198	1198	Score
6.9	6.9	6.9	6.9	6.9	7.0	7.0	7.0	7.0	7.1	7.2	7.3	7.4	7.4	7.4	7.4	7.4	7.5	7.7	9.4	9.4	11.6	100.0	100.0	100.0	Query Match Length
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Aaw59459 Microbial			(L		7	-		Aab95788 Human pro	Human	Prote		Human	Amino	-		Human	Aao08972 Human pol	Lacto	Aag93290 Human pro	Human	Human	Human	Human	Aam40223 Human pol	Description

Novel nucleic acids and polypeptides, useful as central nervous system injuries.

for treating disorders such

Example 5; SEQ ID NO 3368; 10078pp; English

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26
79.5	80	80.5	80.5	80.5	80.5	80.5	80.5	81.5	81.5	81.5	82.5	83	83	83	83	83	83	83	83
6.6	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.8	6.8	6.8	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9
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Aab53428 Human col	Aae21310 Mouse Mrg			_		_		Novel	Esche										

ALIGNMENTS

AAM40223;

22-OCT-2001

(first entry)

AAM40223 standard;

protein;

229

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RESULT 1
AAM4023
IID AAM44
XX
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AAM4023
AC AAM4
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Huma
DE Huma
XX
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Huma
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21-JAN-2000; 2000US-00488725.
25-AFR-2000; 2000US-0059317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00652191.
19-CCT-2000; 2000US-00652191.
19-CCT-2000; 2000US-0063193.
29-NOV-2000; 2000US-0063193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 3368.
                                                                                                                                                                                                                                                              Tang YT, Liu C, Asundi V, Wang J, Wang Z, Wehrman T, Zhou P, Goodrich R, Drmana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                            WPI; 2001-442253/47.
N-PSDB; AAI59379.
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Yang Y,
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Zhang
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, Zhao QA;
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RESULT 2
ABG34656
ID ABG3
XX ABG36
AC ABG3
XX Homa
XX Huma
XX Huma
XX Homo
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Best Local
                                                                                                                                         WPI; 2002-382963/41.
N-PSDB; ABK70506.
                                                                                                                                                                                                                                                                                  Raitano
                                                                                                                                                                                                                                                 Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2000; 2000US-0228432P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2001; 2001WO-US026838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer related protein encoded by cDNA 85P1B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinal inhabin activity, chemotactic/chemokinetic activity, haemostatic and therapy.
                                                                                                                                                                                                                                                                                                                                                  (AGEN-) AGENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200218578-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG34856;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 229
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100.0%; Pred. No. 5.;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                  Hubert
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Composition for modulating the status of 85P1B3 protein or a molecule comprising a substance e.g. antibody specific to, nucleic acid encodion ribozyme of 85P1B3.

encoding

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22-OCT-2001 AAM42009;

(first entry)

RESULT 3 AAM42009

AAM42009 standard; protein; 231 AA.

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                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is the 85P1B3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suspected of having cancer and for monitoring 85P1B3 in a biological sample from a patient who has or who is suspected of having cancer. gene for 85P1B3 is located on human chromosome 15q14. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a composition comprising a substance that modulate the status of 85P1B3, where the status of a cell expresses 85P1B3 gene product is modulated. Also included are a composition comprising a peptide region of 5 amino acids of the 85P1B3 protein,
                                                                                                                                                                                                                                                                                                                                                                            Local Sim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 34; Fig 2; 201pp; English
         181
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                                                                                                                        121 VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKWVCYLLKTKAIV
                                                      181
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                                                                                                                                                                                                                   61 AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                           NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229
NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN
                                                                                                                                                                                   AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL
                                                                                      VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV
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                                                                                                                                                                                                                                                                                                                                                                       Score 1198; DB 5;
Pred. No. 5.2e-127;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as planeimer's, Parkinson's disease, Huntington's disease, amyotrophic plateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as
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19-JUL-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                     and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded polypeptides (AAM38642-AAM42213) with nootropic,
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                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                         231
                                                                                                                                                       MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP
VGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKWVCYLLKTKAIV
                                                           AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL
                                                                                      AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL
                                                                                                                                     MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP
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2000US-00552317.
2000US-00598042.
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s system; neuropathy; central no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO 6940; 10078pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system
                                                                                                                                                                                                                                                                                                                             specification
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Drmanac RT;
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Pred. No. 5.3e-127;
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LA
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Yang Y,
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Zhang
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Zhao QA;
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cc modulate the status of 85P1B3, where the status of a cell expresses cc modulate the status of 85P1B3, where the status of a composition cc 85P1B3 gene product is modulated. Also included are a composition cc comprising a peptide region of 5 amino acids of the 85P1B3 protein, in cc comprising a peptide region of 5 amino acids of the 85P1B3 protein, in cc cmy whole number increment up to 229 that includes an an position cc endytophilicity profile, an an position having a value greater than 0.5 in the cc composition having a value greater than 0.5 in the protein accessible residue profile, an an aposition having a value greater than 0.5 in the sylvancial color of the hydropathicity profile, an an aposition having a value greater than 0.5 in the beta-turn profile; a cc polynucleotide that encodes analogue peptide of 8, 9, 10 or 11 contiguous cresidues of the 85P1B3 protein; a recombinant protein comprising the cc animal that produces an antibody specific to the 85P1B3 protein; a recombinant protein comprising the cc animal that produces antibody that binds to the 85P1B3 protein; a vector comprising a polynucleotide that comprises the variable domains of the heavy and monoclonal antibody specific to the protein; a vector comprising a polynucleotide that encodes the whb; inhibiting growth of cancer cells or treating a patient who bears cancer cells that expresses the protein, antisense polynucleotide to the polynucleotide, cc ribozyme that cleaves the polynucleotide to the polynucleotide, cc ribozyme that cleaves the polynucleotide and T cells that expresses cc comprises an antibody specific to the gromamalian immune response to the protein exposing cells of the mammalian immune system to comprise the protein exposing cells of the mammalian immune system to comprise the protein exposing cells of the mammalian immune system to comprise the protein exposing cells of the mammalian immune system to confide the formulation and caposition.

Cc delivering a cytotoxic agent conjugate. The methods are useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition for modulating the status of 85P11 comprising a substance e.g. antibody specific
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Jakobovits
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Best Local :
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                                                  clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA enable the production of the full length enriched cDNA enable the production of the full length without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                              830 Primers useful for synthesizing full length cDNA clones and
                                                                                                                                                                                                                                                                                                                   The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                        in genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-2000; 2000EP-00114089
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                                form part or Life mat directly from
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su A, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3550; 1380pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                   manipulation.
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2000JP-00183765
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EPO
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82.1%;
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Pred. No. 5.6
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K, Kojima
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Query Match

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Score

113;

DВ

4

Length 233;

Sequence 233

expression

protein

The present sequence is a human protein. The human protein, preferably originated from tumour cell line, is applicable as a drug, a reagent for studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The human protein coding the screening proteins for binding low molecular weight drugs. The human

for

ng proteins for binding low molecular weight drugs. The human coding sequence is useful for gene diagnosis and gene therapy, ion vectors and transformant cells for detection of ligands and

The present sequence is a human protein originated from tumour cell line, is apported in a studying intracellular protein networks a

Sequence

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RESULT 6
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10-FEB-2000; 2000JP-00034090: 
10-FEB-2000; 2000JP-000354091: 
14-FEB-2000; 2000JP-00035829: 
14-FEB-2000; 2000JP-00035899: 
14-MAR-2000; 2000JP-00071161: 
30-MAY-2000; 2000JP-00160851:
                                                                                                                   Human protein originated from tumor cell line, applicable as drug, reagent for studying intracellular protein networks and protein so for drug screening, also encoded cDNA for gene diagnosis and gene
                                                                                                                                                                        WPI;
                                                                                           Claim 1; Page 303-304;
                                                                                                                                                                                          Kato
                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                             06-DEC-1999;
06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene therapy; tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHLAWDLSR-SLGAVVFSRYTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LSWVASQEDTNCILLRCVSCNVSVDKEQKLSKREKENGCVLETLCCAGCSLNLGYVYR
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rches 88;
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RESULT 7
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Best Local
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Query Match
Best Local Similarity
                                                                            The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent wo200177334 (published 18-OCT-2001) which is available in electronic format directly from wIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2003
16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB54167 standard;
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                                                                                                                                                                                                                                                                                                    Bolotine
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                                   Sequence
                                                         ftp.wipo.int/pub/published_pct_sequences.
standardise OS field)
                                                                                                                                                                                                                                                    nucleotide sequence useful in
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                                                                                                                                                                                                                   ID NO 869; 2504pp; French.
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(first entry)
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Pred. No. 0.00075;
0; Mismatches 88;
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                                                                                                                                                                                                                                                         the identification
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                Length 695;
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RESULT 8
AAO08972
ID AAO0
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA008972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA008972 standard; protein;
                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The prolynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating e.g. stem cell growth factor activity immunormodulatory activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous
                                                                          activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 22864; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                             N-PSDB; AAI88903.
                              treatment of cancer, leukaemia, nervous system disorders, arth inflammation. Note: The sequence data for this patent did not of the printed specification, but was obtained in electronic for the printed specification, but was obtained pct_sequences directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                and treating
                                                                                                                                                                                                                                                                                                  Isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LGTIIF-----FYSGTPFFSGAKGELKSRKPAMMMLITMGTTVAY-AYSVYÄTIMSLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 LGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG
                                                                                                                                                                                                                                                                                                                                                                            TY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system
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    269
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                                                                                                                                                                                                                                                                              leic acids and e.g. leukemia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                   polypeptides, inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269
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                                                                                                                                                                                                                                                                                                   useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                      immune
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                                                                                                                                                                                                                                                                                      preventing diagnosing disorders.
                                                                   not form part
                                                                                       arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195
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Query Match
Best Local Sin
Matches 52;

Similarity

7.5%; Score 90; 23.0%; Pred. No.

26;

Mismatches

74;

Indels

74;

Gaps

11;

0

.38;

DB 4;

Length 269;

Conservative

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RESULT 9
AAB93182
AID AAB9
XX AAB9
XX AAB9
AX AAB9
AX AAB9
AX Huma
XX Huma
XX Homo
PN EP10
XX Homo
XX Homo
PN 29-J
PF 28-J
PF 28-J
PF 27-A
PF 09-J
XX WPI;
PT Ishi
XX WPI;
AX HEI
XX Clai
XX Clai
XX Clai
XX Com;
CC Com;
CC Com;
CC Com;
CC Spec
CC Spec
CC Spec
CC Spec
CC Spec
CC Gen;
CC Spec
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of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence'3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                             nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a
                                                                                                                                                                                                         complementary strand of a polynucleotide which comprises one of the 5602
                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the
                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                          diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                         Primer
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HELI-)
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                                                                                                                                                                                                                                                                                                                                                                          ength
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                                                                                                                                                                                                                                                                                                                                          sets for synthesizing polymucleotides, particularly the 5602 full-
cDNAs defined in the specification, and for the detection and/or
sis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAALRGHFCLS----SDKWVCYLLKTKAIVNASEMDIQNVPLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA
                                                                                                                                                                                                                                                                                                    NO 12128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection; diagnosis; antisense therapy; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ
                                                                                                                                                                                                                                                                                           2537pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQPFCHLYWGCTRTGCYGCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto
T;
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RESULT 10
ABB97233
AD 97897
XX ABB97
XX ABB97
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XX Human
XX Human
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                                                                                                                                                                                      An isolated polynucleotide for treating
                                                                                                                                                                           encoded
                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2000; 2000US-00659671
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; antianaemic; vulnerary; antiinflammatory; immunomodu
antiinfertility; cerebroprotective; cytostatic; rheumatic;
neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                      (-ESYH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200222660-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonuclectides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                        Å,
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                                                                                                                                                                                                                                                                                                 Liu
Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRRQAAQPPH----CPAPEGEPGAPQALGDAPPTSVSLTTAVQDYVCPLQGSHALCTCCFQ
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                                                                                                                                                                                                                                                                                                 Zhou P,
Wehrman
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Pred. No. 1.8;
26; Mismatches
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                                                                                                                                                                                                                                                                                               Zhang
RT;
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                                                                                                                                                                s associated sclerosis.
                                                                                                                                                                                                                                                                                                                   Zhao
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The present invention provides the protein and coding novel human proteins. These were isolated from express (ESTs). They can be used to stimulate cell growth, to haematopoiesis e.g. to treat aplastic anaemia, to help

from expressed sequences growth, to regulate mia, to help tissue regrowth

0 f

444

treatment,

to regulate the immune

system

e.g.

to

Example

2; SEQ ID NO 501;

509pp;

English.

invention

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RESULT 11
AAB93168
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Best Local S
Matches 52
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                                                                                                                                                                                                                    29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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                                                                                                                                                              Ota T,
Ishii
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                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001
                                                                                                                                                                                                                                                                                          28-JUL-2000;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602
                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                        Claim
                                                                                                                                        WPI;
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t, Sugiyama
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                                                                                                                                                                                                 HELIX RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                          sequence SEQ
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T, Wakamats
                                                           12100;
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                                                                                                                                                                                                                                                                                                                                                                                     diagnosis;
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Pred. No.
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A, Nagai K,
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1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combin of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
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                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                  FHAR1; RING finger protein; cancer;
                                                                                                                                                                                                                                                                                14-JUN-2001
                                                                                                                                                                                                                                                                                                                     WO200142430-A1
                      New FHAR1 polypeptide,
                                                                                                                                                                                                    08-DEC-1999;
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                                                           AAF89709
                                                                                                                                                               SMITHKLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                     Chaturvedi
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Pred. No. 1.9;
26; Mismatches
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      of the RING
and for use
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                                                                                                                           Hurle
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        finger protein family in anti-cancer vaccine
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Best Local
                          Halazonetis T,
                                                                                                                             29-JUL-1999;
                                                                             (WIST-) WISTAR
                                                                                                                                                                              14-JUN-2000; 2000WO-US016391
                                                                                                                                                                                                                                      08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Checkpoint with forkhead associated domain and ring finger; Chfr; human; mitosis; cell cycle; tumour; diagnosis; antitumour; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through detection of mutations in the associated gene, and for chromosome localization studies, and tissue expression studies. FHARI antibodies are useful to isolate and to identify clones expressing the polypeptides, or to purify the polypeptides by affinity chromatography and to treat cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 664 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents a FHAR1 polypeptide, which is a member RING finger protein family. FHAR1 is useful in the treatment of cer, and as a vaccine for inducing an immunological response in a mal. FHAR1 polynucleotides may also be used as a diagnostic respent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579 IVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 ALAALRGHFCLS-----SDKMVCYLLKTKAIVNASEMDIQNVPLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 PMPDRRAEREQDPRVAPQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 HRSRCATPPRGDFC-----GGTERAIDQA-----SFTTSMEWDTQVVKGSSPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SIGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (checkpoint with
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                                                                        INST ANATOMY & BIOLOGY.
                                                                                                                           99US-0146194P
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                          Scolnick D;
                                                                                                                                                                                                                                                                                                                                                               580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303.
                                                                                                                                                                                                                                                                                                                              <sup>/</sup>note≃ "Met in U2OS cells"
                                                                                                                                                                                                                                                                                                                                                                                    'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Forkhead-associated_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .103
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23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .346
                                                                                                                                                                                                                                                                                                                                                                                 "cysteine-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ring_finger-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89; DB : Pred. No. 2; 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FHA and ring finger) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---QCAVC---LQPFCHLYWGCTRTGCYGCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which is a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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chfr gene (see AAF30352) in human cancer is theorized to underlie the increased sensitivity of cancer cells to antimitotic drugs. Polypeptides acids 31-103, 303-346 and/or 476-641 of this sequence, are claimed methods of determining the tumourigenic potential of a cell comprise examining the cell for the presence of Chfr-mediated ubiquitin-protein ligase activity (in both upon exposure to microtic stress). A diagnostic kit for detecting the tumourigenic potential of a cell cases, absence of expression indicating predisposition to tumourigenesis tumourigenic potential of cell cases, absence of expression indicating predisposition to tumourigenesis tumourigenic potential of cell cells comprises may comprise a ligand that are identified by monitoring their effect on Chfr expression, and are used to retard the growth of cancer cells
Sequence
                                                                                                                                                                                                                                                                                                                                                               naving a torkhead associated domain (FHA) and a ring finger domain. The protein is required for regulation of the transition of cells from prophase to metaphase during mitosis. It has ubiquitin-protein ligase activity. The Chfr checkpoint was evident in primary human cells, but we inactivated in 4 of 8 human cancer cell lines. In U2OS cells, a mutatior was identified that caused a Val to Met amino acid substitution in the highly conserved C-terminal Cys-rich region of the Chfr protein. In the absence of the Chfr checkpoint, cells subjected to mitotic stress condensed their chromosomes despite failing to separate their chromosomes. Chfr may monitor centrosome separate to separate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid sequence of mitotic checkpoint gene encoding a checkpoint with forkhead-associated domain and ring finger protein, diagnosing tumorigenic cells and in screening for anticancer drugs.
                                                                                                                                                                                                                                                                                                                                             chromosomes. Chfr may monitor centrosome separation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8(a);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is that of human
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664 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forkhead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig 4A-C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associated domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitotic checkpoint
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             a mutation
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Best Local
                          molecular weight marker; food supplement; antiparkinsonian; nootropic;
                                                                                   ulcers;
                                                                                                      neurodegenerative diseases; anaemia; platelet disorder; wound;
                                                                                                                                            Human; diagnostic; drug screening; forensics; biodiversity assessment; Parkinson's disease;
neuroprotective; antianaemic; anticoagulant; thrombolytic;
                                                                                                                                                                                                                                                                     Human novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC32818 standard; protein;
                                                                                                                                                                                                                                                                                                                                             18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                     ADC32818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
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                                                                    osteoporosis; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SIGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMPDRRARREQDPRVAPQ------QCAVC---LQPFCHLYWGCTRTGCYGCLA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRSRCATPPRGDFC-----GGTERAIDQA----SFTTSMEWDTQVVKGSSPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR--
                                                                                                                                                                                                                                                  contig-encoded polypeptide sequence, SEQ ID NO:2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1245
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74;
                                                                                                                                                gene mapping;
Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
                                                                                                          burns;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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identification of mutations methods of peventing, treating or and/or monoclonal antibodies for carrying out the methods of the invention. The invention; methods for the identification of compounds of the control of the invention; methods for the identification of compounds that modulate the expression or activity of the polymucleotide and/or polymediate the contig sequences corresponding to the cDNA sequences of the invention of (ADC31861-ADC32627) and the polymediates encoded by the contigs (ADC32628 -ADC33394). The nucleic acids and polymeptides of the invention are cuseful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are calso used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polymeptides
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang TY,
Zhou P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADC32051.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primers, and in the recombinant production of a protein. The polypeptide are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a human contigencoded polypeptide sequence used in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Wang D,
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ABU23878
contributions of the sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(C (1) a vector comprising a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense curleic acid; (4) a host cell containing the vector; (3) an isolated continued are:

(C antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular crompound that influences the activity of a gene in an operor required for proliferation; (7) identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation of identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product its compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene context of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001; 2001US-00815242
06-SEP-2001; 2001US-00948993
25-OCT-2001; 2001US-0342923P
08-FEB-2002; 2002US-0362699P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2002; 2002WO-US009107
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Xu HH;
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Search completed: July 20, 2004, 11:16:29 Job time: 56 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 669 AA;
                                                                                 466 LNIKSISDLYRITKE 480
                                                                                                                        205 LTHNRLKSLMKILSE 219
                                                                                                                                                                        423 HL
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Minimum DB
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
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US-08-882-704A-6
US-09-155-158-6
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US-09-018-576-3
US-09-018-576-3
US-09-248-137-3
US-09-248-137-12
US-09-248-137-12
US-09-252-991A-19049
US-09-252-991A-19049
US-09-18-520-933-3
US-09-18-520-933-3
US-09-18-520-933-3
US-09-18-520-933-3
US-09-18-520-933-3
US-09-18-530-88-18-36
US-08-105-868-36
US-08-105-868-36
US-08-105-868-36
US-08-105-868-36
US-08-105-868-31
US-08-840-062-6
US-08-840-062-6
US-08-840-062-6
US-08-804-227C-14
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US-08-804-198-2
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Compugen Ltd.
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Patent No. 5268463
Patent No. 5432081
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appli
Sequence 1, Appli
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Sequence 2, Appli
Sequence 3, Appli
Sequence 31, Appli
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Patent No. 5268463
Patent No. 5432081
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NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 08-DEC-1989
PRIOR APPLICATION DATA:

US/07/447,976

APPLICATION NUMBER: 119,102

RESULT 2 5268463-7 5268463 ; Patent No. 5268463 ; Patent Promoter a-GLUCURONIDASE GENE ; TITLE OF INVENTION: PLAANT PROMOTER a-GLUCURONIDASE GENE ; CONSTRUCT ; NUMBER OF SEQUENCES: 9 ; NUMBER OF APPLICATION DATA:	1 Similarity 26.5%; Pred. No. 0.12; 40; Conservative 27; Mismatches 54; Indels 30; Gaps 87 LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYN	4-000C-6596 4-000C-6596, Application US/09134000C No. 6617156 LINFORMATION: CANT: Lynn Doucette-Stamm et al OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND REFERENCE: 032796-032 NT APPLICATION UNMBER: US/09/134,000C NT FILING DATE: 1998-08-13 APPLICATION NUMBER: US 60/055,778 FILING DATE: 1997-08-15 R OF SEQ ID NOS: 6812 SR OF SEQ ID NOS: 68	28 75 6.3 717 6 5262177-5 29 75 6.3 1088 4 US-09-920-804-2 30 75 6.3 1088 4 US-09-920-804-4 30 75 6.3 1129 4 US-09-920-804-4 31 75 6.3 2227 3 US-08-734-674-2 32 75 6.3 2227 4 US-09-653-499-4 35 74 6.2 380 3 US-08-801-344-11 36 74 6.2 2109 3 US-08-805-61 37 74 6.2 2109 3 US-08-805-6 38 74 6.2 2109 5 PCT-US96-06053-6 39 74 6.2 2227 3 US-08-80-6 39 74 6.2 2227 4 US-09-653-499-6 40 74 6.2 2227 3 US-08-80-80-6 39 74 6.2 2109 5 PCT-US96-06053-6 40 74 6.2 2227 3 US-08-80-6 39 74 6.2 2227 3 US-08-80-6 39 75 6.1 2227 4 US-09-653-499-6 40 74 6.2 2227 3 US-08-397-232-4 41 74 6.2 2227 4 US-09-653-499-6 42 75 6.1 589 3 US-08-453-848-13 44 73.5 6.1 589 3 US-09-169-027-13 5 Sequence 13, Appl Appl Appl Appl Appl Appl Appl App
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5432081-7
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TITLE OF INVENTION: HOST CELLS T
GLUCORONIDE PERMEASE GENE
NUMBER OF SEQUENCES: 10
CUBRENT APPLICATION DATA.
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Best Local Similarity
Matches 37; Conserv
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APPLICATION NUMBER: 264,
FILING DATE: 31-OCT-1988
;SEQ ID NO:7:
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                                                                                  GENERAL INFORMATION:
APPLICANT: Jeffer
              APPLICANT: Wilson, Katherine J.

APPLICANT: Leader, Michael

TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 456
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FILING DATE: 10-NOV-1987
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FILING DATE: 08-DEC-1989
APPLICATION NUMBER: 264,586
FILING DATE: 31-OCT-1988
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FILING DATE: 15-OCT-1993
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Jefferson, Kıu...
Jenn, Katherine J.
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25.2%; Pred. No. 1.9;
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                                                                                    Richard A.
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RESULT 5
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LENGTH: 457 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: NO. 5879906tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                       APPLICANT: Jefferson, Richard A.
Wilson, Katherine J.
Leader, Michael
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                       CITY: Seattle
STATE: Washington
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CLASSIFICATION: <Unknown>
                APPLICATION NUMBER: US/09/151,957 FILING DATE: 11-Sep-1998
                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K--KFKEIVVEIDNRKKVQQQLISDIT 456
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                                                                                                                                                            ZIP: 98104-7092
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(206) 682-601
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                                                                                                                                                                          USA
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US-10-195-158-6
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Patent No. 6659764
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/882,704
FILLING DATE: «UDACHOWN»
ATTORNEY/AGENT INFORMATION:
NAME: No. 6429292tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REGISTRATION INFORMATION:
190106.404
TELEPHONE: (200,622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/195,158
FILING DATE: 08-Aug-2002
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                    ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jefferson, Richard A.
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6659764tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
                                                                                                                                                                               PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317
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                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
                                                                                                               APPLICATION NUMBER: US/09/151,957
FILING DATE: 11-Sep-1998
APPLICATION NUMBER: US 08/882,704
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 457 amino acids
                                                                                                     FILING DATE: <Unknown>
                                                                                                                                                                                  APPLICATION DATA:
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Leader, Michael
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Pred. No. 1.9;
30; Mismatches
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                                                 US-08-342-930-2
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Best Local :
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Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 2034
REFERENCE/DOCKET NUMBER: 2034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,930
APPLICATION NUMBER: US/08/342,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DAVIS, ALAN R. APPLICANT: DIXON, JACK E. TITLE OF INVENTION: OSTEO TITLE OF INVENTION: PHOSPI
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                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                             MOLECULE TYPE: protein
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TELEFAX: 706141
                                                                                                                                                                   TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                            FILING DATE: 21
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
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                                                                                TOPOLOGY:
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                                                                                                             LENGTH:
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37; Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                              1711 amino acids
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   6.7%;
29.6%;
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   Score 80.5;
Pred. No. 19
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US-09-018-576-3
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US-09-018-576-3
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 19. FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, RY60-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                        y match 6.6%;
Local Similarity 23.2%;
hes 56; Conservative 24
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STREET: ...
STREET: ...
STREET: ...
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TELEFAX: 732/594-4720
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                                                                                                                   LISASGOLKIADFGLARVFS---PDGSRLY-THQ--VATRSVGCIMGELLNGSPLPPGKN 187
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Pred. No. 2.5;
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Sequence 3, Application US/09248137 Patent No. 6030788 GENERAL INFORMATION:
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
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TELECOMMUNICATION INFORMATION:
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TOPOLOGY: linear
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ZIP: 07065-0907
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P.O. Box 2000, RY60-30
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CYCLIN-DEPENDENT PROTEIN KINASE
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                                                                                  Sequence 12, Application US/09248137 Patent No. 6030788
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                                                                       GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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                             NUMBER OF SEQUENCES:
                                         APPLICANT: Gerhold, David L.
TITLE OF INVENTION: CYCLIN-DEPENDENT PROTEIN
               CORRESPONDENCE ADDRESS
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ZIP: 07065-0907
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P.O. Box 2000, RY60-30
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732/594-4720
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CYCLIN-DEPENDENT PROTEIN KINASE
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23.2%; Pred. No. 2.5;
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                                               KINASE
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Best Local 9
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                                                                                                    GENERAL INFORMATION:
APPLICANT: Marc J. I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                            Sequence 19049, Application US/09252991A Patent No. 6551795
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                        FILE REFERENCE: 107196.136
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MEDIUM TYPE: Floppy disk
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NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 732/594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                              188 DIEQLCYVLRILGTPNPQVWPELTELPDYNKIS-FKEQVPMP
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                      Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 2.
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187 167 63

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Sequence 3, Application US/08520933
Patent No. 5981194
GENERAL INFORMATION:
APPLICANT: Jefferies, Wilfred A. APPLICANT: McGeer, Patrick L. APPLICANT: Rothenberger, Sylvia APPLICANT: Food, Michael R.
                                                                                                                 RESULT 14
US-08-520-933-3
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US-09-537-682-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NUMBER OF SEQ ID N
; SEQ ID NO 19049
; LENGTH: 190
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TAKEUUHI, Kenichi
APPLICANT: KOIDE, Yoshinao
APPLICANT: NAKANISHI, Yuji
APPLICANT: SUZUKI, Satoru
TITLE OF INVENTION: L-ALPHA-GLYCEROPHOSPHATE OXIDASE GENE,
TITLE OF INVENTION: L-ALPHA-GLYCEROPHOSPHATE OXIDASE GENE,
TITLE OF INVENTION: L-ALPHA-GLYCEROPHOSPHATE OXIDASE GENE
FILE REFERENCE: A20-121814C/KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09537682 Patent No. 6303357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: A20-121814C/KI
CURRENT APPLICATION NUMBER: US/09/537,682
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 2
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Local Similarity 32.9%;
                                                                                                                                                                           203
                                                                                                                                                                                                                                                 120 LVGIEGSLKGSTYNLLFCGSCGIPVGF-----HLYSTHAALAALRGHFCLSSDKMVCYLL 174
                                                                                                                                                                                                                                                                               103 LLPIYEDEGATTFNMF------ŚVKVAMDLYDKLANVTGTKYENYTLTPEEVLEREPF
                                                                                                                                                                                                                                                                                                        66 LPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTN-----NVVLEAPF 119
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                                                                                                                                                                 EGDQIVGVKARDL----LTDEVIEIKSKLVI 229
                                                                                                                                                                                                                                                                                                                                    DFAEGT-----SSRSTKLVHGGIRYLKTFDVEVV--ADTVGERAVVQGIAPHIPKPDPM 102
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   Food, Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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23.2%; Pred. No.
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Pred. No.
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                                                                                                Sequence 3, Application US/09285040 Patent No. 6455494
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                                                                                     GENERAL INFORMATION:
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                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-520-933-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Shona S. McDiarmid
REGISTRATION NUMBER: 38,798
REFERENCE/DOCKET NUMBER: 7685-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,933
FILING DATE: August 31, 1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kennard, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yamada,
APPLICANT: Kennard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                         158 LRGHFCLSSDKMVCYL----LKTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSL 213
                                214 MKILSEVTP 222
                                                                                                                                                                      110 TUNVVLEAPFLVGIEGS--
                                                                                                                                                                                                                                                                                                                                             59;
IQCVSAKSP 384
                                                              MKGLLC-DPNRLPPYLRWCVLSTPEIQKCGDM-
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                         LN----EGQRLFSHEGSSFQMFSSEAYGQKDLLFKDSTSELVPIATQTYEAWLGHEYLHA
                                                                                                                                                                                         TLPSWGQALLSQDFELLCRDGSRADVTEWRQCHLARVPAHAVVVVRADTD----GGLIF-RL 276
                                                                                                                                                                                                                         QLPSWLQP------ERCAVFQCAQCH--AVLADSVHLAWDLSRSLGAVVFSRV 109
                                                                                                                                                                                                                                                               RGDSSG--EGVCDKSPLERYYDYSGAFRCLAEGAGDVAFVKHSTVL-----
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L. Malcolm
Use of p97 and Iron Binding Proteins
as Diagnostic and Therapeutic Agents
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                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                            -AVAFRRQRLKPE
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                                                                                                                                                                                                                                                                 -ENTDGK 220
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                          375
                                                                                                                            332
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McGeer, Patrick L. Rothenberger, Sylv Food, Michael R.

Sylvia

Jefferies, Wilfred A.

Kennard, Malcolm

Yamada,

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TELEFAX: 416-361-1398;
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-040-3
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Search completed: July 20, 2004, 11:10:45 Job time: 21 secs
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FILING DATE: 01-APR-1999
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7685
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416.364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: USE
TITLE OF INVENTION: as
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                    110 TNNVVLEAPFLVGIEGS----LKGSTY---NLLFCGSCG--IPVGFHLYST---HAALAA 157
                                                                                      376 IQCVSAKSP 384
                                                                                                                                                                          333 MKGLLC-DPNRLPPYLRWCVLSTPEIQKCGDM-
                                                                                                                                                                                                                158 LRGHFCLSSDKMVCYL----LKTKAĮVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSL 213
                                                                                                                                                                                                                                                                                                                                                221 TLPSWGQALLSQDFELLCRDGSRADVTEWRQCHLARVPAHAVVVRADTD---GGLIF-RL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                      171 RGDSSG--EGVCDKSPLERYYDYSGAFRCLAEGAGDVAFVKHSTVL-----ENTDGK 220
                                                                                                                               214 MKILSEVTP 222
                                                                                                                                                                                                                                                                277 LN----EGORLFSHEGSSFOMFSSEAYGOKDLLFKDSTSELVPIATOTYEAWLGHEYLHA 332
                                                                                                                                                                                                                                                                                                                                                                                           65 QLPSWLQP-----ERCAVFQCAQCH--AVLADSVHLAWDLSRSLGAVVFSRV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 RGDFCGGTERAIDQASFTTSMEW------DTQVVKGSSPLGPAGLGAEEPAAGP 64
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0
seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
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1 MAAQPLRHRSRCATPPRGDF.....LKSLMKILSEVTPDQSKPEN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1285356 segs, 312560742 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                July 20, 2004, 11:09:23; Search time 46 Seconds (without alignments)
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Published_Applications_AA:*
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Copyright (c) 1993 - 2004 Compus
             /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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SUMMARIES

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7.2	7.3	7.4	7.4	7.7	7.7	8.0	9.4	9.4	11.5	11.6	100.0	100.0	100.0	100.0	Query Match I
669	848	435	664	695	361	708	233	233	29	164	229	229	229	229	Query Match Length DB
12	16	16	9	15	16	16	16	10	10	10	10	10	10	10	BB
US-10-282-122A-51802	US-10-437-963-155606	US-10-437-963-186569	US-09-780-525-2	US-10-369-493-18389	US-10-437-963-154548	US-10-437-963-195427	US-10-408-765A-969	US-09-890-688-82	US-09-942-052-704	US-09-942-052-707	US-09-942-052-731	US-09-942-052-730	US-09-942-052-729	US-09-942-052-728	ID
Sequence 51802, A			sequence 2, Appli	Sequence 18389, A	Sequence 154548,	sequence 19542/,	Sequence 969, App	Sequence 82, Appr		10,	731,	/30,	129,		Description

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61 AAGPOLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL 120

45	44	43	42	41	40	e e	38	37	36	35	3 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
. 78	78	78.5	78.5	78.5	78.5	78.5	78.5	78.5	79	79	79	79.5	79.5	90	80	81		81.5		81.5				82.5	83	83.5	84	84	8
ი ა	6.5	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.7	6.7	6.8	6.8	6.8	ტ. 8	6.8	6.9	6.9	6.9	6.9	6.9	7.0	7.0	7.0	7.1
162	162	1563	1259	855	591	452	452	373	482	482	339	212	212	544	305	859	1969	457	457	278	1043	502	325	278	663	888	1902	295	337
15	14	12	16	16	16	12	9	12	15	14	16	10	9	12	14	12	16	14	13	12	15	12	16	12	12	16	16	12	14
US-10-292-798-1320	US-10-017-161-1656	-10-282-	-10-43/-963-10289	-10-437-963-14844	0-437-963-	US-10-403-161-8	161A-	US-10-425-114-39137	-10-229-541A	US-10-160-764-81	US-10-437-963-124922	US-09-925-299-968	968	ᅩ	US-10-183-116-59	δ	4.	-518-	-158-	US-10-425-114-66220	369-493-	US-10-424-599-226730	~	•	- 1	0-437-963-14789	US-10-437-963-139559	-10-424-599-22350	US-10-156-761-10954
sequence 1340, Ap		1757	U 107070	Sequence 14844/,	sequence 195425,	sequence a, Appri	Sequence 23/, App	sequence 3913/, A		α 1 .			96			0,0			Sequence 6, Appli		9793, 1		Sequence 2, Appli		e 515/3,	6 14/87		e 22350	10954

ALIGNMENTS

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US-09-942-052-728
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APPLICANT: Ge, WANGMAO
APPLICANT: Challita-Edd, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028-00
CUGRENT APPLICATION NUMBER: US/09/942,052
CUGRENT APPLICATION NUMBER: 60/228,432
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
PRIOR FILING DATE: 2000-08-28
SEQ ID NO 728
SEQ ID NOS: 744
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 728
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 728, Application US/09942052 Publication No. US20030170626A1 GENERAL INFORMATION:
                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 229; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Raitano, Arthur B. APPLICANT: Faris, Mary APPLICANT: Hubert, Rene S. APPLICANT: Afar, Daniel
                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Unknown Organism: 85P1B3/OIP5 OTHER INFORMATION: clone A protein
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                FEATURE:
                              1 MAAQPLRHRSRCATDPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGABEEP 60
MAAQPIRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP 60
                                                                                                          0;
                                                                                                             Score 1198; DB 10;
Pred. No. 7.7e-117;
Nismatches 0;
                                                                                                                  Indels
                                                                                                                                                                  Length 229;
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US-09-942-052-730
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                     APPLICANT: Raitano, Arth
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
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                                                                                                         Sequence 730, Application US/09942052
Publication No. US20030170626A1
GENERAL INFORMATION:
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Afar, Daniel
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
TITLE OF INVENTION NUMBER: US/09/942,052
CURRENT APPLICATION NUMBER: US/09/942,052
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR APPLICATION NUMBER: 60/228,432
NUMBER OF SEQ ID NOS: 744
NUMBER OF SEQ ID NOS: 744
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Publication No.
     APPLICANT:
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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Hubert, Rene S.
Afar, Daniel
Ge, Wangmao
Challita-Eid, Pi
                                                                                                                                                                                                                                   NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVTPDQSKPEN 229
                                                                                                                                                                                                                                                                                                                                                                                                      AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09942052
D. US20030170626A1
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                                                                                         Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1198; DB 10; 100.0%; Pred. No. 7.7e-117;
 Pia M
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                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
PRIOR FILING DATE: 2001-08-28
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 731
                                                                            Matches
                                                                                                Best Local
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 731, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER

EILE REFERENCE: 51158-20028 00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 730
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Best Local :
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APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Raitano, APPLICANT: Faris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                    LENGTH: 229
TYPE: PRT
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Unknown Organism: 85P1B3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Unknown Organism FEATURE:
                                                                              229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229;
                    1 MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFL
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                                                                                             Similarity
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MAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hubert,
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arthur B.
                                                                    100.0%; Score 1198; DB 10; 100.0%; Pred. No. 7.7e-117; tive 0; Mismatches 0;
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Pred. No. 7.7e-117;
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                                                                                                          DB 10;
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US-09-942-052-707
Sequence 704, Application US/09942052
Publication No. US20030170626A1
GENERAL INFORMATION:
                                                          RESULT 6
US-09-942-052-704
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SEQ ID NO 707
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT FILINGLATION NUMBER: US/09/942,052
CURRENT APPLICATION NUMBER: US/09/942,052
PRIOR APPLICATION NUMBER: 60/228,432
PRIOR FILING DATE: 2001-08-28
PRIOR FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Raitano, Arth
APPLICANT: Faris, Mary
APPLICANT: Hubert, Rene
APPLICANT: Afar, Daniel
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (67)
OTHER INFORMATION: Unknown
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LOCATION: (50)...(51)
OTHER INFORMATION: Unknown
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OTHER INFORMATION: Unknown
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LOCATION: (44)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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LOCATION: (93)
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LOCATION: (67)
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                                                                                                                                                                                                                                     Local
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                                                                                                                                                                162 FCLSSDKWVCYLLKTKAIVNASEMDIQNVPLSEKIAELK 200
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Afar, Daniel
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                                                                                                                                                                                                                     Conservative
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                                                                                                                                        YLLKTKAIVNASEMDIONVPLSEKIAEVK 35
                                                                                                                                                                                                                   11.6%; Score 138.5; DB 10. 82.1%; Pred. No. 4.4e-06; tive 1; Mismatches 1;
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APPLICANT: Mihoro SAEKI
TITIE OF INVENTION: Human Proteins and cDNAs thereof
FILE REFERENCE: 2001-1102A/MMC/00653
FURRENT APPLICATION NUMBER: US/09/890,688
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: UT 11-346863
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: UP 11-34684
PRIOR APPLICATION NUMBER: UP 2000-31062
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 2000-02-08
PRIOR FILING DATE: 2000-02-10
PRIOR PRILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: UP 2000-34091
PRIOR APPLICATION NUMBER: UP 2000-34090
PRIOR APPLICATION NUMBER: UP 2000-35829
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR PRILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: UP 2000-35899
PRIOR APPLICATION NUMBER: UP 2000-35899
PRIOR APPLICATION NUMBER: UP 2000-35899
PRIOR APPLICATION NUMBER: UP 2000-71161
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US-09-890-688-82
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                                                                                       ; ORGANISM: Homo
US-09-890-688-82
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SEQ ID NO 704
SENGTH: 29
TYPE: PRT
ORGANISM: Unknown Organism
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PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 744
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20028.00
CURRENT APPLICATION NUMBER: US/09/942,052
CURRENT FILING DATE: 2001-08-28
Best Local Similarity
Matches 52; Conserv
                                         Query Match
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OTHER INFORMATION: Descript:
OTHER INFORMATION: sequence
                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2000-16085
                                                                                                                                                           LENGTH:
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Similarity 100.0%; Pred. No. 4.3e-07;
29; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                            PatentIn
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    Conservative
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                        9.4%; Score 113; DB 10
27.1%; Pred. No. 0.0034;
    30; Mismatches
                                                     DB 10;
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RESULT 9
US-10-437-963-195427
Sequence 195427, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
PDITCANT: Cao, Yongwei
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US-10-408-765A-969
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NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 969
LENGTH: 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Fahy, Boin D.
APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                     208 NRLKSLMKILSE
                                                                                                                                                                                                                                                                                             154 CTPKNLDYKRDLFCLSVEAIESYVLGSSEKQIV-SEDKELFNL---ESRVEIEKSLTQME 209
                                                                                                                                                                                                                                                                                                                                                                                                    91 VHLAWDLSR-SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLY 149
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                                                                                                                                                                                                                                  DVLKALQMKLWE 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%; Score 113; DB 16;
27.1%; Pred. No. 0.0034;
7ative 30; Mismatches 88;
                                                                                                                                                                                                                                                                     219
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_54398C.1.pep US-10-437-963-154548
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US-10-437-963-154548
; Sequence 154548, Application US/10437963
; Publication No. US20040123343A1
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                                                                                                                                                TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) B CURRENT APPLICATION INVESER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
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US-10-437-963-195427
                       Query Match
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 195427
LENGTH: 708
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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                                                                                                  TYPE: PRT
ORGANISM: Oryza sativa
                                                                                           FEATURE:
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ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 LRHRRKAATPSASDASPPPPRRQSIVTIGEKEARAKAARAKSGGTSSA-----SPTTVST 279
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Wu, Wei
Boukharov, Andrey A
Barbazuk, Brad
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Cao, Yongwei
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Boukharov,
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                  7.7%;
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Score 92; I
Pred. No. 1;
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Pred. No. 1
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            DB 16;
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              Length 361;
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Best Loc Matches

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Similarity 25.3%;

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US-10-369-493-18389
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US-09-780-525-2
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GENERAL INFORMATION:
APPLICANT: Bin-Bing Zhou
APPLICANT: Yuan Zhu
APPLICANT: Priya Chaturve
APPLICANT: Mark R. Hurle
APPLICANT: Xiaotong Li
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18389
LENGTH: 695
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                                                                                              Sequence 2, Application US/09780525 Patent No. US20020004223A1
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APPLICANT: Hin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                  101 LGTIIF---
                                                                                                                                                                                                                                                                                                                                                                 101 LGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APTPLPFRRAVRAKAAQDGSGGTSSASPAVAST----DVVVVPGSREATPSG-PASDPV 102
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                                                                                                                                                                                                 VGDL--LLVKENEKIPADGLILSEALVDES 241
                                                                                                                                                                                                                                                                                                   HF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                 Priya Chaturvedi
Mark R. Hurle
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                                                                                                                                                                                                                                                                                                 ----CLSSDKMVCYLLKTKAIVNASE--MDI----
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 15; Length 695; Pred. No. 2.5;
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LENGTH: 664
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                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT FAPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 186569 LENGTH: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/456,876
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/456,876
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 2
SOFTMARR: PROCESSES
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                                                                                                                           Matches
                                                                                                                                                        Query Match
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                                                                                                                                              Best Local Similarity
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APPLICANT: Kovalic, David
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: PAT_MRT4530_83357C.1.pep
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                                                                APEPLSCRHGRHLRCAAVD--
                                                                                           AAQPL--RH--RSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGA
                            EEPAAGPOLPSWIOPERCAVFOCAOCHA--VLADSVHLAWDLSRSLGAVVFSRVTNNVVL 115
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   EDPSPQPGVPLILLP--
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Zhou, Yihua
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23.0%;
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Pred. No. 4.9;
26; Mismatches 7
                                                                                                                                            Score 88.5;
Pred. No. 3;
   -LCCRCYAKEICSEYVVRTTDLVNHI--
                                                                  --GGAGRETERPSPPAPQ-
                                                                                                                                Mismatches
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                                                                                                                                                                 DB 16;
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                                                                                                                                82;
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                                                                                                                                  Indels
                                                                                                                                                                 Length
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      -LNSNAIS 135
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Sequence 51802, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_55353C.1.pep
US-10-437-963-155606
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US-10-437-963-155606
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Best Local ,
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LENGTH: 848
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Publication No. US20040123343A1
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2003-05-14
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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LOCATION: (1).. (848)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                               GSKAMECGVKMCLVGWPWLAWDELGPRSGYQFGLNHRRPLVKAVLDGHLCEEEDAVNCLP 322
                                                                                                                                                           KLRKTVGSASE----
                                                                                                                                                                                                                                                         ----SCGIPV--
                                                                                                                                                                                                                                                                             YVSCGSVIEMSROMKAARAGVRAQSXPACXGIPTVGKVGSV--LLFTARMGEGLCHMFTT 262
                                                                                                                                                                                                                                                                                                             --SIGAVV-FSRVTNNV-----VLEAPFLVGIEGSLK-GSTYNLLFCG------
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                                                                                                                                                   --AKEAVKPAVKQEKKIRS-VKVLSLVS-DLSLP 363
                                                                                                                                                                                                                                                  GFHLYSTH---AALAALRGHFCLSSDKMVCYL 173
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Search completed: July 20, 2004, 11:15:23 Job time : 47 secs
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; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51802
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 51802
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APPLICANT:
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PRIOR FILING DATE: 2000-11-27
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                                                                                         466
                                                                                                                                                                                       423
                                                                                                                                        205 LTHNRLKSLMKILSE
                                                                                                                                                                                                                147 HLYSTHAALAALRGHFCLGSDKMVCYLLKTKAIVNASEMDIQNVP-LSEKIAE-LKEKIV
                                                                                                                                                                                                                                                                      366 DIGRKKVKIGSRVFVRRSNDVI---PEIMGVTEETEGETNEIEAPTICPYCGSEIVKEGV
                                                                                                                                                                                                                                                                                                                 96 DLSR---SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNL-----LFCGSCGIPVGF 146
                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                  h 7.2%; Score 86.5; 1 Similarity 27.4%; Pred. No. 9; 37; Conservative 22; Mismatches
                                                                                      LNIKSISDLYRITKE
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Forsyth, R.
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Yamamoto, Robert
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ck, Robert
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DNA (cytosine-5-)-	probable uvid - My	hypothetical proce	endotherial monocy	gryceror denydroge	probable UNA (cyco	cbb8c procein (uso	formate denydrogen	cellulase - Fibrob	probable acyl-coa	gryceror-3-phospha	melanotransierin	TonB-dependent rec	nypothetical proce	versican precursor	trwC protein homol

ALIGNMENTS

copper-potassium transporting ATPase B copB [imported] - Lactococcus lactis subsp. lactis C.Species: Lactococcus lactis subsp. lactis C.Species: Lactococcus lactis subsp. lactis C.JDate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: C86731 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehr Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: C86731

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A;Status: preliminary A;Molecule type: DNA A;Residues: 1-695 <STO>

Science 281, 375-388, 1998 A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71250; MUID:98332770; PMID:9665876 A;Accession: D71293 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA	C;Accession: D/1293 R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwrson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mcrthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.	RESULT 2 D71293 B71293 probable phosphoribosylglycinamide formyltransferase - syphilis spirochete probable phosphoribosylglycinamide formyltransferase - syphilis spirochete C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999	Db 214 VGDLLLVKENEKIPADGLILSEALVDES 241	Qy 196 IAELKEKIVLTHNRIKSLMKILSEVTPDQS 225 ; ; ; ; ;	Db 154 HMGMNFWFELATLIVIMLIGHLIEMKÄIMGÄGDALKDLASLVPKKAHLKSGKDVELSELK 213	Qy 161 HFCLSSDKMYCYLLKTKAIVNASBMDIQNVPLSE-K 195	Db 101 LGTIIFFYSGTPFFSGAKGELKSRKPAMMMLITMGITVAY-AYSVYATIMSLNG 153	_	Query Match 7.7%; Score 92; DB 2; Length 695; Best Local Similarity 25.3%; Pred. No. 2.2; Matches 38; Conservative 28; Mismatches 50; Indels 34; Gaps 7;	A;Gene: copB A;Gene: copB C;Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding	A;Residues: 1-695 <sto> A;Cross-references: GB:AE005176; PID:g12723778; PIDN:AAK04949.1; GSPDB:GN00146 A;Experimental source: strain IL1403 C:Genetics:</sto>

A;Residues: 1-597 <COL>
A;Cross-references: GB:

source:

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Ranamycin kinase (EC 2.7.1.95) - Campylobacter
c;Species: Campylobacter jejuni
C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1
C;Accession: A43623
R;Tenover, F.C.; Gilbert, T.; O'Hara, P.
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A;Cross-references: EMBL:AL137561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-306 < AA
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A; Accession: T46399
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T46399
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                                                                                                                                                        ALAALRGHECLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE
                                                                                                                              LVÄLQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE
                                                                                                                                                                                        PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNML
                                                                                                                                                                                                               ----SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTY-NLLFCGSCGIPVGFHLYSTHA 153
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                                                                                                                                                                                                                                                                                                                                HRSRCATPPRGDFC-----GTERAIDQA----SFTTSMEWDTQVVKGSSPL-----
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se: strain Nichols
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28.0%;
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O'Hara,
                                                                                                                                                                                                                                                                                                                                                                ; Score 89; DB; Pred. No. 1.5; 26; Mismatches
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Pred. No. 2
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                        11-Feb-1993 #text_change
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A; Accession:

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glutamate synthase (NADH2) (EC 1.4.1.14) precursor [validated] - alfalfa C;Species: Medicago sativa (alfalfa) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 03-Jun-20 C;Accession: JQ1977; pQ0551
R;Gregerson, R.G.; Miller, S.S.; Twary, S.N.; Gantt, J.S.; Vance, C.P. Plant Cell 5, 215-226, 1993
                                                                                                                                                          RESULT
JQ1977
A; Title: Molecular characterization of NADH-dependent glutamate A; Reference number: JQ1977; MUID:93200806; PMID:8453303
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C;Superfamily: polydeoxyribonucleotide synthase (NAD+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.;
Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAD-dependent DNA ligase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: A97229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE001437; PIDN: AAK80620.1; PID: g15025704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-669 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A96900; A; Accession: A97229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-250 -TEN-
A;Cross-references: GB.M29953; GB:J03316; NID:g144186; PIDN:AAA76822.1; PID:g144187
C;Superfamily: kanamycin kinase
C;Keywords: phosphotransferase
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A;Title: Nucleotide sequence of a novel kanamycin resistance A;Reference number: A43623; MUID:89387451; PMID:2550983
A;Accession: A43623
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                                                                                                                                                                                                                                                                                                                                                                                                              96 DLSR----LFCGSCGIPVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 LSSDKMVCYLLKTKAIVNA----SEMDIQNVPLSEKI-AELKEKIVLTHNRLKSL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 VESRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG-HFC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 CFIDHPIKYI----ECLVNALHQLQAIDIRNCPFSSKIDVRLKELKYLLDNRIADI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 IFSKTTYSVKREAEMMWLSDKLKVPDV-----IBYGVREHSEYLIMSELRGKHID
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33; Conserv
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27.4%; Pred. No. 6.8;
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Pred. No. 1
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                                                                                       #text_change 03-Jun-2002
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A;Molecule type: mRNA
A;Residues: 1-2194 <GRE>
A;Cross-references: GB:L01660; N
A;Accession: PQ0551
A;Molecule type: protein
A;Residues: 102-114 <GR2>
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AB2074
AB2074
Eferrichrome binding protein of ABC transporter all2147 [imported] - Nostoc sp. C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: glutamate synthase (NADH)
C;Reywords: 3Fe-4S; chloroplast; iron-sulfur protein; metalloprotein; NAD; oxidoreductas
E;1-101/Domain: propeptide #status predicted <PRO>
F;10-2104/Product: glutamate synthase (NADH) #status experimental <MAT>
F;102/Active site: Cys #status predicted
F;1246,1252,1257/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA Res. B, 205-211, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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R; Kaneko, T.; Nakamı
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C; Superfamily:
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                                                                                                                                                       ISHALGKVKIPLKPQRVVVLEENIILDSVLALGVK-
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  LGLTWLKSSYKILSSIAP
                                         LTHNRLKSLMKILSEVTP
                                                                                                                      GFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIVNASEMDIQNVPLSEKIAELKEKIV
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24.7%;
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26.1%;
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  181
                                                                                                                                                                                                                                                 Score 84.5; D. Pred. No. 4.8; 7; Mismatches
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Pred. No.
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42;
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09-Dec-2002
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126 61

SLKGSTYNLLFCGSC--GIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIVNAS

183

118

-AITLNERGVAVKCDLCIDRDKPLCVMVCPKGALSES

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A;Gene:
C;Superf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     formate hydrogenlyase, iron-sulfur subunit 2 - Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec:1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Genome Sequence and Comparative Analysis of the A; Reference number: A96900; MUID:21359325; PMID:21359325
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A;Cross-references: GB:AE001437;
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                                                                                                                                                   A;Gene: MTH1736
C;Superfamily: n:
F;62-118/Domain:
                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: B69099
                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Smith,
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A;Residues: 1-143 <MTH>
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J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                               A;Cross-references:
                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.; Breton, G.; Omelchenko, M.V.;
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                                   PERCAVFOCAOCHAVLADSVHLAWDLSRSLGAVVF-----
PELCD--ECMKCERICPKNAIRVID----
                                                                                                                                                 nrfC protein; ferredoxin 2[4Fe-4S]
n: ferredoxin 2[4Fe-4S] homology <F</pre>
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                                                                                            6.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 83;
Pred. No.
                                                                                            Score 82.5; D. Pred. No. 2.3;
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Smith, D.R.
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14;
     -GVPVFCMHCSPERAPCLNICPEDAIVEVDG
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ATCC824
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                                       -SRVTNNVVLEAPFLVGIEG
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;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, I trett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. bmitted to GenBank, April 2001 jbmitted to GenBank, April 2001 jbescription: Sulfolous solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
Molecule type: DNA
Residues: 1-329 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ansport protein, probable [imported] - Sulfolobus solfataricus
Species: Sulfolobus solfataricus
Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.8%; Score 81.5; Best Local Similarity 22.2%; Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                Matches
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Accession: D90404
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                                                 167 DKMVCY-LIKTKAIVNASEMDIQNVPISE---KIAELKEKIVLTHNRIKSIMKIISEVTP 222
                                                                                                                                                                     117 APFLVG-----IEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSS 166
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                                                                                                                 93 VRFLVGVIFGLLTSYAVESAVKSGRNVLVGFTTAGWPIGWVI---
                                                                                                                                                                                                                               33 LSESMHLÄYWEVFAIVALPFLGRIIGSFIYQVFKNSVISYCFPFLGFLVILQNFLGALIF 92
                                                                                                                                                                                                                                                                                         87 LADSVHLA-WD------LSRSLGAVVFSRVTNNVV------
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-SYVAYVLLKNWNVINISGILIMLLALFELNGKEFGERSKISVSFPRLTSILIYVSALTP 193
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, i; Rose, D.J.; Mau, B.; Shao, Y. ience 277, 1453-1462, 1997
Title: The complete genome sequence of Escherichia coli K-12.
Reference number: A64720; MUID:97426617; PMID:9278503
Accession: B64918 }ene: uidB; gusB Superfamily: melibiose carrier protein .ccuronide permease uidB - Escherichia coli (strain K-12)
Species: Escherichia coli
Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
accession: B64918 Experimental ross-references: GB:AE000257; GB:U00096; NID:g1787898; PIDN:AAC74688.1; PID:g1787902; experimental source: strain K-12, substrain MG1655 Residues: 1-457 <BLAT> Molecule type: DNA Status: nucleic acid sequence not shown; translation not enetics:

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C;Keywords: carrier protein; transmembrane protein F;37-53/Domain: transmembrane #status predicted <TM01>F;81-97/Domain: transmembrane #status predicted <TM02>F;152-168/Domain: transmembrane #status predicted <TM03>F;184-200/Domain: transmembrane #status predicted <TM04>F;231-247/Domain: transmembrane #status predicted <TM05>F;231-247/Domain: transmembrane #status predicted <TM05>F;263-279/Domain: transmembrane #status predicted <TM07>F;408-424/Domain: transmembrane #status predicted <TM07>F;408-424/Domain: transmembrane #status predicted <TM08>
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  RESULT 15
H85767
H85767
C;Species: Escherichia coli (strain 0157:H7, substra: C;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85767
C;Accession: H85767
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, R;Perna, N.T.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.;
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C;Superfamily:
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: AAY
A;Rosidues: 1-457 < <AAY
A;Cross-references: GB:BA000007; PIDN:BAB35746.1; PID:g13361790; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A; Reference number: A99629; MUID:21156231; PMID:11258796
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DNA Res. 8, 11-22, 2001
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Matches 37
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a, N.T.; Plunkett III, G.; Burland, V.; L.; Grotbeck, E.J.; Davis, N.W.; Lim,
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37; Conserv
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                                                                                                                                                                                       K--KFKEIVVEIDNRKKVQQQLISDIT
                                                                                                                                                                                                                                          KIAELKEKIVLTHNRLKSLMKILSEVT
                                                                                                                                                                                                                                                                               QAIG---GSIPAFILGLSGYIANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIWFYPLTD
                                                                                                                                                                                                                                                                                                                      IPVGFHLYSTHAALAALRGHFC--LSSDXWVCYLLKTKAIVNASEMDIQNV-----PLSE 194
                                                                                                                                                                                                                                                                                                                                                                                                    WDLSRSLGAVVFSRVTNNV------VLEA-----PFLVGIEGSLKGSTYNLL-FCGSCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melibiose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 81.5;
Pred. No. 12
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M.; Shinagawa, H.
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A;Cross-references: GB:AE005174; NID:g12515601; PIDN:AAG56604.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85767
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                                                                                                                                                                                                                                                              A;Gene: uidB
C;Superfamily: melibiose carrier protein
                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-457 <STO>
                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary A;Molecule type: DNA
맑
                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                Local
                               195
                                                                375
                                                                                                                                317 WSLPVALVALAIASIGOGVTMTVMWALEADTVEYGEYLTGVR--IEGLTYSLFSFTRKCG
432
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                                                                                                                                                                                                                Similarity
                                                              QAIG---GSIPAFILGLSGYIANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIWFYPLTD
                                                                                             IPVGFHLYSTHAALAALRGHFC--LSSDKWVCYLLKTKAIVNASEMDIQNV-----PLSE
                                                                                                                                                               WDLSRSLGAVVFSRVTNNV-----VLEA-----PFLVGIEGSLKGSTYNLL-FCGSCG
 K--KFKEIVVEIDNRKKVQQQLISDIT
                             KIAELKEKIVLTHNRLKSLMKILSEVT 221
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                              6.8%;
                                                                                                                                                                                                  30;
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Search Job tim time : 18 secs completed: July 20, 2004, 11:18:11

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Minimum DB :
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Maximum Match 100%
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Perfect score:
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seq length: 2000000000
      SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_numan:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_vordent:*
12: sp_virus:*
13: sp_vertebrate
14: sp_virus:*
16: sp_bacteriap:
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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1198
1 MAAQPLRHRSRCATPPRGDF.....LKSLMKILSEVTPDQSKPEN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1017041 seqs, 315518202 residues
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sp_organelle:*
sp_phage:*
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sp_virus:*
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength	BI	ID	Description
1	122	10.2	218	11	Q9CXR6	Q9cxr6 mus musculu
2	115.5	9.6	204	11	Q9CZJ6	Q9czj6 mus musculu
ω	92	7.7	361	10	Q8S611	Q8s611 oryza sativ
4	92	7.7	695	16	Q9CH87	Q9ch87 lactococcus
ហ	91	7.6	652	4	Q96EP1	Q96ep1 homo sapien
ወ	90.5	7.6	597	16	083693	O83693 treponema p
7	89	7.4	306	4	Q9NT32	Q9nt32 homo sapien
80	89	7.4	623	4	Q9NVD5	Q9nvd5 homo sapien
9	89	7.4	652	4	Q96SL3	Q96sl3 homo sapien
10	89	7.4	664	4	Q9NRT4	Q9nrt4 homo sapien
11	87.5	7.3	663	11	Q8BJZ9	Q8bjz9 mus musculu
12	87	7.3	664	11	Q810L3	Q81013 mus musculu
13	86.5	7.2	669	16	Q97FQ5	Q97fq5 clostridium
14	86	7.2	145	16	Q839T4	Q839t4 enterococcu
15	85	7.1	337	16	Q82HU1	Q82hu1 streptomyce
16	85	7.1	671	5	Q815K5	Q8i5k5 plasmodium

ť	Д	44	43	42	41	40	39	ω 80	37	36	ω G	ω 4	ω G	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17
ć	20	80	80.5	80.5	81	81	81	81	81.5	81.5	81.5	81.5	81.5	82	82	82.5	82.5	82.5	82.5	83	83	83	83.5	84	84	84	84.5	84.5	85
			6.7				6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8				6.9	6.9	6.9				7.0	7.0	7.0	7.1	7.1	7.1
,	431	105	768	766	1697	1697	443	418	2172	672	563	457	329	2216	967	640	493	423	143	663	579	475	800	1947	1129	496	740	361	2194
,	16	16	10	10	12	12	10	13	Ŋ	11	11	16	17	10	16	12	10	16	17	16	12	10	9	10	16	4.	4.	16	10
# C	0881119	Q8FNE5	Q8VZC5	023161	Q8QZF9	Q8QZF6	Q8LPK8	07ZYY0	Q7X4R4	Q80V27	Q99KM1	Q8X673	Q97W97	Q9LV03	Q9A2U2	056294	023213	Q87AI1	027769	Q97JS8	Q8BEN6	Q7XQK5	Q7Y5U5	Q84SE8	Q7UKD4	096SL8	Q8IWD2	Q8YV34	Q40360
	_	Q8fne5 corynebacte				Q8qzf6 crimean-con			m	Q80v27 mus musculu										Q97js8 clostridium		Q7xqk5 oryza sativ	Q7y5u5 bacteriopha	Q84se8 oryza sativ		Q96s18 homo sapien		4	medicago

ALIGNMENTS

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RESULT 2

POCCASE

ID COCCASE

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                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
EMBL; AK012533; BAB28302.1; -
MGD; MGI:1913828; 2610039C10Rik.
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9CZJ6;
                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 LYSTHAALAALRGHFCLSSDKMVCYLL------KTKAIVNASEMDIQNVPLSEKIAE
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                                                                                                                                                                             Similarity
DSVHLAWDLSR-SLGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFH 147
                                                   DSSRYLRLOKWAN--MSSADALGLEKERPEEKAAAAENP-
                                                                                           DQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAVLA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKEKIVLTHNRLKSLMKILSEVTPDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSSRYLRLQKWAN--MSSADALGLEKERPEEKÄÄAAENP-----LVFLCARCRRPLG
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                                                                                                                                                                                                                                                  204 AA;
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                                                                                                                                                                                                                                               22949 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                            9.6%; Score 115.5; DB 11 25.6%; Pred. No. 0.0035; tive 29; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24447 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pred. No. 0.00087;
80; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                             BBD667250FDF9B0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55390E5BFDDDE8C2 CRC64;
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                                                                                                                                                                                                                                                                                                                                           mouse
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                                                                                                                                                                                         DB 11; Length
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                                                                                                                                                                                                                                                                                                                                      cDNA collection.";
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                                                                                                                                               Indels
                                              -----LVFLCARCRRPLG
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                                                                                                                                                                                              204;
                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                    Wilming L.,
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                                                                                                                                          Gaps
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                                                 64
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                   267 L
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STRAIN-cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AC099400; AAL91599.1; -. EMBL; AE017047; AAP51763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund C.,
Wing R.A., Yu Y., Oates R., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; NCBI TaxID-29447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-CCT-2003 (TrEMBLrel. 25, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saski C., Henry D., Oates
"Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative gypsy-type retrotransposon protein. OSJNBA0096E22.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cience 300:1566-1569(2003).
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204 V 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 LYSTHAALAALRGHECLSSDKMVCYLL--KTKALVNASEMDIQNVPLSEKIAELKEKIVL 205
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                             EAPFLVGIEGSLKGSTYNLL--FCGSCGI-----PVGFHLYSTHAALAAL----RGH
                              AARIGEEMSNRIYIGACHILACVRLAH-PELDLREILDQGEASDARKDVMEEVGDLGKSV
                                                                    FCLSSDKM-----VCYLLKTKAIVNASEMDIQNV-----
                                                                                                                                                                                     AGRGSPAAVLSWEELQVEMGRLLEAGA--RVIGREIAEARGLEHRM----SELGNN---
                                                                                                                                                                                                                          AGPQLP----SW--LQPERCAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVL 115
                                                                                                                                                                                                                                                                    APTPLPFRRAVRAKAAQDGSGGTSSASPAVAST
                                                                                                                                                                                                                                                                                                  AAQPIRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8S611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRCTPKNIDYKRDLFCLSVEAVESYTIGSSEKQİV-SEDKELFNL---ESRVEIEKSİKQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAR-2002) to
                                                                                                                                                                                                                                                                                                                                                                                                                       361 AA; 38805 MW;
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                        -LSEIRGSLR-VTYTGLHQLAGKCGIKSTIPANPDEFSLTSSLAELAAAMEEIPSKH
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                                                                                                                                                                                                                                                                                                                                                                 25.3%;
                                                                                                                                                                                                                                                                                                                                                                                     7.78;
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                                                                                                                                                                                                                                                                                                                                           ; Score 92; DB; Pred. No. 1.6; 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity,
                                                                                                                                                                                                                                                                                                                                                                                                                     F883BB3E8B8FFF45 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consortium;
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                                                                                                                                                                                                                                                                -DVVVVPGSREATPSG-PASDPV
                                                                                                                                                                                                                                                                                                                                                                               Length 361;
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                                                                    ----PLSEKIAELKEKI
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                              266
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RESULT
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Best Local S
Matches 38
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GO; GO:0015622; F:ATP binding; IEA.
GO; GO:0015622; F:ATPase activity; coupled
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0030000; P:metabolism; IEA.
GO; GO:0030000; P:metabolism; IEA.
GO; GO:0030000; P:metabolism; IEA.
InterPro; IFR006403; ATPase-IB Cu.
InterPro; IFR0064103; ATPase-IB E2.
InterPro; IFR006415; ATPase E1-E2.
InterPro; IFR008150; E1-E2 ATPase reg.
InterPro; IFR008250; E1-E2 ATPase; 1.
Pfam; PF00122; E1-E2 ATPase; 1.
Pfam; PF00122; Hydrolase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence (lactis ssp. lactis II1403"; Genome Res. 11:731-753(2001). EMBL; AE006319; AAK04949.1; -. PIR; C86731; C86731.
                                                                                     Q96EP1;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S.,
Weissenbach J., Ehrlich S.D., Soro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copper-potassium transporting ATPase B. COPB OR LL0851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (St. Bacteria; Firmicutes; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=IL1403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=1360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0119;
                       Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                   Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00154; ATPASE_E1_E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGAVVFSRVTNNVVLEAPFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRG
                                                                                                                                                                                                                                                                                              VGDL--LLVKENEKIPADGLILSEALVDES
                                                                                                                                                                                                                                                                                                                                          IAELKEKIVLTHNRLKSLMKILSEVTPDQS
                                                                                                                                                                                                                                                                                                                                                                                      HMGMNFWFELATLIVIMLIGHLIEMKAIMGAGDALKDLASLVPKKAHLKSGKDVELSELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGTIIF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR01511; ATPase-IB1 Cu;
TIGR01525; ATPase-IB hvy;
TIGR01494; ATPase_P-type;
      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       695
                                                                                       (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                           protein. (Human).
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATATPASE
    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P., Mauger S., Jaillon O., Malarme K., ich S.D., Sorokin A.; sequence of the lactic acid bacterium Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- FYSGTPFFSGAKGELKSRKPAMMLTIMGITVAY-AYSVYATIMSLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                             CLSSDKMVCYLLKTKAIVNASE--MDI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                       Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92; DB 1
Pred. No. 3.7;
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
      Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B4947C3C2A0FA0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Streptococcus lactis) les; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEA.
                                                                                                                                                                                    652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEA
                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                          225
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                                                                                                                 update)
         Hominidae;
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                                                                                            update)
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                                Euteleostomi;
         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
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Best Local S
Matches 53
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PROSITE; PS00
PROSITE; PS50
PROSITE; PS50
Hypothetical |
SEQUENCE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00240; FHA; 1.
SMART; SM00184; RING; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000253;
InterPro; IPR008984;
InterPro; IPR001841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: CONTAINS 1 RIN EMBL; BC012072; AAH12072.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                            MEDLINE-9833//0; FULLWHELL CO., Sutton G.G., Fraser C.M., Norris S.J., Weinstook G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Dodson R., Gwinn M., Hickey E.K., Chalzberg S., Peterson J. Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback McDonald L., Artiach P., Bowman C., Cotton M.D., Pujii C., Garlar McDonald L., Artiach P., Bowman C., Cotton M.D., Pujii C., Garlar McDonald L., Artiach P., Bowman C., Cotton M.D., Pujii C., Garlar McDonald L., Artiach P., Bowman C., Cotton M.D., Pujii C., Garlar McDonald E., Reconstruction M.D., Fujii C., Garlar M.D., Pujii C., Gar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Phosphoribosylglycinamide formyltransferase, puta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00498; FHA; 1.
Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     083693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum.
Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        083693
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98332770; PubMed=9665876; Fraser C.M., Norris S.J., Weinsto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Nichols;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=160;
                                                                                            EMBL; AE001243; AAC
PIR; D71293; D71293
                                                                                                                      Science 281:375-388(1998).
EMBL; AE001243; AAC65662.1;
                                                                                                                                                                               "Complete genome spirochete.";
                                                               TIGR;
                                                                                                                                                                                                                                               Venter J
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                               GO:0016740;
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                                                               TP0695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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P8500518; ZF_RING_1; 1.

P850089; ZF_RING_2; 1.

ical protein; Metal_binding; Zinc; Zinc-finger.

652 AA; 72058 MW; 1A50773CEA679F07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRRQAAQPPH---CPAPEGEPGAPQALGDAPSTSVSLTTAVQDYVCPLQGSHALCTCCFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .acenta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALAALRGHFCLS----SDKMVCYLLKTKAIVNASEMDIQNVPLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFCELNLGDKCLDGVLNNNSYESDILKNYLAT-RGLTWKNMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLGPAGLGAE-EPAAGPQLPSWLQPERCAVFQCAQCHAVLADSVHLAWDLSR-
                                                                                                                                                                                                                                                  .c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMPDRRVEREQDPRVAPQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AUG-2001) to the EMBL/GenBank/DDBJ databases.
      IPR003135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A.
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                                   F:transferase activity;
                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SMAD_FHA.; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.6%;
      ATP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spirochaetales;
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      -grasp
                                                                                                                                                                                                                      of.
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Pred. No. 4.3;
Pred. Mismatches
                                                                                                                                                                                                                      Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            597
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                                                                                                                                                                                                                   pallidum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spirochaetaceae; Treponema
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01-OCT-2000
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Mammalia; Eutheria;
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Transferase; Complete proteome.
SEQUENCE 597 AA; 63325 MW;
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                                                                                                                                                    ALAALRGHFCLS-----SDKMVCYLLKTKAIVNASEMDIQNVPLSE 194
                                                                                                              LVALQRGVFLLSDYRVTGDTVLCYCCGLRSFRELTYQYRQNIPASE
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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23.0%; Pred. No. 2.
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28.0%; Pred. No. 4
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EMBL/GenBank/DDBJ databases.
  PRT;
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Q96SL3
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A Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.
A Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wal
A Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
L Submitted (FEB-2000) to the EMBI/GenBank/DDBJ databases.
C -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
R EMBL; AKOO1658; BAA91817.1; -.
R InterPro; IPR000253; FHA.
R InterPro; IPR000894; SMAD FHA.
R InterPro; IPR001841; Znf_ring.
R FFAM. BEDAGAGE. EFFA. 1 f _ ring.
                                                                                                                                                                                                                                                                                                               Q96SL3;
Q96SL3;
01-DEC-2001;
01-DEC-2001;
01-OCT-2003;
SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Saisokai T., Nagai K., Sugano S., Actsuka S., Yoshikawa Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ14781.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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01-OCT-2000
01-OCT-2000
01-OCT-2003
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein FLJ10796.
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Pred. No.
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Aotsuka S., Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                     652
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                                                                          Wakamatsu
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Best Local S
Matches 52
PROSITE; PS500518;
PROSITE; PS00518;
PROSITE; PS50089
Metal-binding; Z
  InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001841; Znf_ring.
Pfam; PF00498; FHA; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00240; FHA; 1.
SMART; SM00184; FHA; 1.
SMART; SM00184; FHA DOMAIN; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50009; ZF RING 1; 1.
PROSITE; PS50009; ZF-RING-2; 1.
Metal-binding; Zinc; Zinc-finger
SEQUENCE 664 AA; 73386 MW; 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSNRT4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cell cycle checkpoint protein CHFR.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Bukaryota; Metazoa; Chordata; Craniata; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50006; FHA DOMAIN; 1.

PROSITE; PS00518; ZF RING 1; 1.

PROSITE; PS50089; ZF RING 2; 1.

PROSITE; PS50089; ZF RING 2; 1.

Hypothetical protein; Metal-binding; Zinc; Zinc-
SEQUENCE 652 AA; 72030 MW; 572F2CE6D1743D80
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SMART; SM00184; RING; 1
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Pfam; PF00097; zf-C3HC4; 1.
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InterPro; IPR008984; SMAD_FHA.
InterPro; IPR001841; Znf_ring.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20388685; PubMed=10935642;
Scolnick D.M., Halazonetis T.D.;
                                                                                                                                                                                                                                                                                               PDB; 1LGQ; 07-AUG-02.
Genew; HGNC:20455; CHFR.
GO; GO:0007093; P:mitotic checkpoint;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       metaphase.";
Nature 406:430-435(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NRT4
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; AK027687; BAB55297.1; -.
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Nature 420:563-573(2002).
EMBL; AK077629; BAC36912.1; -...
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00240; FHA; 1.
SMART; SM00184; RING; 2.
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Mammalia; Eutheria;
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PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
SEQUENCE 663 AA; 73855 MW;
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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1. 25, Last annotation update)
checkpoint protein CHFR.
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26; Mismatches
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19; Mismatches
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166

-SDKMVCYLLKTKAIVNASEMDIQNVPLSE

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RESULT 12
Q810L3
ID Q810L
ID Q810L
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DT 01-JU
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Best Local S
                                                                                                                                                                                                                                                                                                              Q97FQ5 PRELIMINARY;
Q97FQ5;
01-OCT-2001 (TremBirel 18, C
01-OCT-2001 (TremBirel 25, L
01-OCT-2003 (TremBirel 25, L
           SEQUENCE FROM N.A. STRAIN=ATCC 824 /
                                                                                                              NCBI_TaxID=1488;
                                                                                                                                               Clostridium.
                                                                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia;
                                                                                                                                                                                                                                                              CAC2673
                                                                                                                                                                                                                                                                                        NAD-dependent DNA ligase.
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PROSITE; PS50060; FHA DOMAIN; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
PROSITE: PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003
01-JUN-2003
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00240; FHA; 1.
SMART; SM00184; RING; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD FHA.
InterPro; IPR001841; Znf_ring.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC043792; AAH43792.1; -.
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Q810L3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNNYESDILKNYLAT-RGLTWKSVL---
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           DSM 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%; Score 87; DB
22.1%; Pred. No. 11;
7ative 20; Mismatches
/ VKM B-1787;
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                     Clostridiales; Clostridiaceae;
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RESULT 14
Q839T4
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R PIR; A97229; A97229.

R GO; GO:00016022; C:intracellular; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0003911; F:DNA ligase (NAD) activity; IEA.

DR GO; GO:0016874; F:ligase activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006281; P:DNA replair; IEA.

GO; GO:0006281; P:DNA replication; IEA.

GO; GO:0006810; P:transport; IEA.

Thiarpro; IPR001157; BRCT.

Thiarpro; IPR001157; BRCT.
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Best Local
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SMART; SM00278; HbH1; 3.

SMART; SM00278; LIGANG; 1.

TIGREAMS; TIGR0575; dnl; 1.

PROSITE; PS50172; BRCT; 1.

PROSITE; PS01056; DNA LIGASE N2; 1.

PROSITE; PS00216; SUGĀR TRANSPORT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003583; HHH 1.

InterPro; IPR008994; Nucleic acid C
InterPro; IPR008929; Sug_transporte
InterPro; IPR005829; Sug_transporte
InterPro; IPR004149; Znf DNAligase
Pfam; PP00533; BRCT; 1.

Pfam; PP01653; DNA ligase N; 1.

Pfam; PF03120; DNA ligase OB; 1.

Pfam; PF03119; DNA ligase ZBD; 1.

Pfam; PF03119; DNA ligase ZBD; 1.

Pfam; PF03119; DNA ligase ZBD; 1.
                                                                                                                                                           01-JUN-2003
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                               Q839T4;
                                           Enterococcus faecalis (Streptococcus faecalis)
Bacteria; Firmicutes; Lactobacillales; Enteroco
NCBI_TaxID=1351; [1]
                                                                                                          Hypothetical EF0068.
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SEQUENCE 669 AA; 75900 MW; A4A4C9CAB72767DF CRC64;
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubbis J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
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InterPro; IPR001679; DNA1
InterPro; IPR004150; DNA
InterPro; IPR000445; HhH.
                                                                                                                                                                                                                                                                                                                                                                                                                   466
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                                                                                                                                                                                                                                                                                                                                                                                                                LNIKSISDLYRITKE
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                                                                                                                                                      (TremBirel. 24, Created)
(TremBirel. 24, Last seq
(TremBirel. 24, Last ann
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                    protein.
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Znf_DNAligase_C4.
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DNA_ligase_OB.
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                                                                                                                                                                                                                                                                                                                                                                                                                480
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                                                                                                                                                        sequence update) annotation updat
                                                                                                                                                                                                                                                                      145
                                              Enterococcaceae;
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                                              Enterococcus
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RESULT 15
Q82HUID Q82HU
ID Q82HU
DT 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 01-UID 0
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Matches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical SEQUENCE 1.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative tryptophanyl-tRNA TRPS1 OR SAV3417.
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  microorganism Streptomyces avermitilis.";
mat. Biotechnol. 21:526-531(2003).

EMBL; AP005035; BAC71129.1; -
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004830; F:tryptophan-trNA ligase activity; I
GO; GO:0006436; P:tryptophanyl-trNA aminoacylation;
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
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                                                                                                                                                                                                                                                                                                                                                                                                                     avermitilis: deducing
metabolites.";
                                                                                                                                                                                                                                Ikeda H., Ishikawa J., Hanamoto A., Shinose
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / MEDLINE=22608306; PubMed=12692562;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21477403; Pu
Omura S., Ikeda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MA-4680
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145 AA; 16506 MW; 81A8B6D4A7F8CE17 CRC64;
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13; PubMed=11572948;
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Pred. No. 1.9;
27; Mismatches
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                                                                                                                                                                                                                     analysis of the industrial
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                                                                                         IEA.
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PROSITE; PS00178; AA TRNA LIGASE_I; 1.
Aminoacy1-trNA synthetase; Complete proteome.
SEQUENCE 337 AA; 37096 MW; 23DAF4D121131864 CRC64;
                                                                                                                                                                                                                                                                                                                   InterPro; IPR002306; Trp_tRNA-synt_lb. Pfam; PF00579; tRNA-synt_lb; 1.
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                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                              Match
  191
                         181
                                                  131
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                                                                                                                                                                            18 GDFCGGTER--AIDQASFTTSMEWDTQVVKGSSPLGPAGLGAEEPAAGPQ-LPSWLQPER
                                                                                                                           75
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                                                                                                                                                                                                                   Similarity
                                                                                                                           CAVFQCAQCHAVLADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS----
                                                                                                                                                    NASEMDIQ--NVPLSEKIAELKEKIVLTHNRLKSLMKILSEVT
                                                 TYPVLQVADILLYQANEVPVGEDQRQHIELTRDLAERFNGRFGETFTVPKPYILKETAKI
                                                                          TY-----NLLFCGSCGIPVG----FHLYSTHAALAALRGHFCLSSDKMVCYLLKTKAIV
                                                                                                  CTLF--VQSH--VPEHAQLAWIMNCLTGFGEASRWTQFKDKSAK-----QGADRASVGLF
 ----FDLQDPSIKMSKSASTPKGLINLLDEPKATAKKVKSAVT
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                  7.1%;
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34; Mismatches
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11;

Search completed: July 20, Job time : 42 secs 2004, 11:17:44

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Scoring table:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CA1C MOUSE
YN06 SYNEL
POL2 BAMMU
CE11 CAEEL
PTPV RAT
IDS2 YEAST
KUGD OCEIH
PTPV MOUSE
PFTB ARATH
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P16735 human cytom
Q9kpw2 vibrio chol
Q891i1 clostridium
P52453 human herpe
P08582 homo sapien
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RX MEDLINE=22388257; PubMed=12477932;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Bistchenko L., Marusina K., Farner A.A., Rubin G.M., Hong L.,

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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Blakesley A.C., Grinwood J., Schmutz J., Myers R.M.,

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Matches 229; Conserv
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Gene 247:215-232(2000).
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GO: GO:0005515; F:protein binding; GO: GO:00075154; p:cell communication GO: GO:0007154; p:cell communication GO: GO:0007154; p:cell communication GO: GO:0007154; p:cell communication GO: GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communication GO:0007154; p:cell communic
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A Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
A Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
A Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
A Holroyd S., Hornsby T., Howarth S., Hickle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
A Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
A Holroyd S., Hornsby T., Jones M., Leather S., McDonald S., McLean J.,
A James K., Jones M., Jones M., Jones M., Sheltet D., Odell C.,
A Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
A Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
A Mutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
A Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
A Melljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
A Melljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
A Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
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Best Local S
Matches 52
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C970.12 in chromosome
SPCC970.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
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EMBL; BC042917; AAH42917.1; -.
Genew; HGNC:1286; C21orf45.
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
SIMILARITY: TO S.POMBE C970.12.
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between the Swiss Institute of Bioinformatics and the I the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to licenseaich air
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein 2 [Contains: Helper component
(EC 3.4.22.45) (HC-Pro); 70 kDa protein]
Barley mild mosaic virus (strain ASL) (BaNNY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                -i- CATALYTIC ACTIVITY: Hydrolyzes a Gly- |-Gly bond at it terminus, commonly in the sequence -Tyr-Xaa-Val-Gly- | processing of the potyviral polyprotein.
-i- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand
                                                                                                                                                                                       (BaMMV).";
Eur. J. Plant Pathol. 100:233-241(1994).
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=103899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                               SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                    complete nucleotide sequence of RNA2 of
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B_SPombe; SPCC970.12;
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                                                                                                                                                                                                                                                      Kuehne T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equires a license agreement (S email to license@isb-sib.ch).
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                                                                                                                                       TO PEPTIDASE FAMILY C6
                 noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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01-JAN-1990 (Rel. 13, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Aminoglycoside 3'-phosphotransferase (EC 2.7.1.95) (Kanamycin kinase, type VII) (Neomycin-kanamycin phosphotransferase, type VII)
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                                                                                                                                                                                                                                                                                                                                  P14508;
                                    phosphotransferase genes.";
plasmid 22:52-58(1989).
-i- FUNCTION: RESISTANCE TO KANAMYCIN AND
AMINOGLYCOSIDES, INCLUDING AMIKACIN.
                                                                                      Tenover F.C., Gilbert T., O'Hara P.;
"Nucleotide sequence of a novel kanamycin resistance from Campylobacter jejuni and comparison to other kar
                                                                                                                                         SEQUENCE FROM N.A. STRAIN=PS1178;
                                                                                                                                                                                         Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                        type VII) (Ne (APH(3')VII).
                                                                                                                            MEDLINE=89387451; PubMed=2550983;
                                                                                                                                                                                                                    Plasmid
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SIMILARITY:
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                                                                                          kanamycin
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                                                                                                      gene,
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Matches 33
                                                                                                                     Ikeda H., Ishikawa J., Hanamoto A., Shinose M Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative ana microorganism Streptomyces avermitilis.", Nat. Biotechnol. 21:526-531(2003).

-i- CATALYTIC ACTIVITY: ATP + L-tryptophan +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYW1 STRAW
Q82HU1;
15-MAR-2004
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss_Institute of Bioinformatics and the EMBL outstation -
                                                        diphosphate + L-tryptophanyl-trna(Trp).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-I aminoacyl-trna synthetase family.
                                                                                                                                                                                                                  STRAIN=MA-4680 / ATCC 31267 / NCIM
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                        Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Oson Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptom avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21477403; PubMed=11572948; Cmura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces avermitilis. Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1) (TrpRS 1).
TRPS1 OR SAV3417.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomycineae; Streptomycetaceae;
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1) (TrpRS 1).
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15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibiotic resistance; Transferase; Kinase; ATP-binding; Plasmid. ACT_SITE 178 178 BY SIMILARITY. SEQUENCE 250 AA: 29680 MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M29953; AAA76822.1; -.
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      ween the European
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   Swiss Institute
Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                     / ATCC 31267 / NCIMB 12804 / NRRL 8165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43, Created)
43, Last sequence update)
43, Last annotation update)
43, Last annotation update)
43, Synthetase 1 (BC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                                                                                                                                                                                                                                                Sci. U.S.A. 98:12215-12220(2001).
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ycetaceae; Streptomyces
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Pred. No.
                                                                                                                                                                                                                                    NCIMB 12804 / NRRL 8165;
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Best Local S
Matches 55
                                                                                                                                                                                                                    Plant Cell 5:215-226(1993)
                                                                                                                                                                                                                                                                   alfalfa nodules."
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 102-114.
MEDLINE=93200806; PubMed=8453303;
Gregerson R.G., Miller S.S., Twary S.N., Gar
                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago sativa (Alfalfa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids ; Fabales; Fabaceae; Papillonoideae; Trifolieae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q03460;
01-OCT-1993 (Rel. 27,
01-OCT-1993 (Rel. 27,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                       Gregerson R.G., Miller S.S., Twary S.N., Gant
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3879;
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InterPro; IPR002305; tRNA-synt 1b.
InterPro; TRNA-synt I.
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_lb, 1
Pfam; Pf00579; tRNA-synt_lb; 1.
PRINTS; PR01039; TRNASYNTHTRP.
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                                                                oxoglutarate + NADH.

COPACTOR: Binds a 3Fe-4S cluster; FAD and FM PATHWAY: Glutamine Synthetase/GOGAT pathway withe assimilation of ammonia.

SUBCULIULAR LOCATION: AMYLOPLAST (POTENTIAL).
                   TISSUE SPECIFICITY: Root nodules.
SIMILARITY: TO OTHER GLUTAMATE SYNTHASES
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Mismatches 100;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006982; Glu_synth_centr.
InterPro; IPR006981; Glu_synth NTN.
InterPro; IPR002932; Glu_syntha_sub1.
InterPro; IPR006005; Glut_syntha_sub1.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR0001103; Pyridine_redox_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGR01317; GOGAT_sm_gam; 1.
Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NAD; Chloroplast; Amyloplast; Transit peptide; Glutamate biosynthesis.
                     POL2_BAMMN STANDARD; PRT; 891 AA.
PB9684;
PB9684;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein 2 [Contains: Helper component
(EC 3.4.22.45) (HC-Pro); 70 kDa protein].
Barley mild mosaic virus (strain Na1) (BaMMY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; JQ1977; JQ1977
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  Viruses; ssRNA positive-strand
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n; PF000770; Pyr redox; 1.
VTS; PR00419; ADXRDTASE.
VTS; PR00368; FADPUR.
VTS; PR00361; PNDRDTASEI.
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GLUTAMINE AMIDOTRANSFERASE ()
FMN (BY SIMILARITY).
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IRON-SULFUR (3FE-4S) (BY SIM.
IRON-SULFUR (3FE-4S) (BY SIM.
IRON-SULFUR (3FE-4S) (BY SIM.
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Pred. No.
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    no
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    DNA stage;
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(BY SIMILARITY).
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       Potyviridae;
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RESULT 9

UIDB ECOLI

TD TUIDB ECOLI

AC P30868; P77457;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUC-1993 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 40, Last annotation update)
DE Glucuronide carrier protein (Glucuronide perme GN UIDB OR GUSB OR UIDB OR B1616.

OS Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mild mosaic virus (Na1 strain).";
Arch. Virol. 141:2077-2089(1996).
-!- CATALYTIC ACTIVITY: Hvdrolvze
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SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
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Pred. No. 12;
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PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
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TIGRFAMs; TIGR00792; gph; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
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"The complete genome sequence of Bscherichia coli K-12.";
Science 277:1453-1474(1997).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Riley M., Condon M.A., Rose D.J.,
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Submitted (OCT-1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                      ProDom; F
                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                      InterPro; IPR002660; Herpes_UL6.
Pfam; PF01763; Herpes_UL6; 1.
ProDom; PD003210; Herpes_UL6; 1.
SEQUENCE 640 AA; 74538 MW; 4
                                                                                                                                                                                                                                 EMBL; U43400; AAC54737.1; -. PIR; T41977; T41977.
                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P52455;
01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                           Nicholas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human herpesvirus (type Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virion protein U76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PO-TD
                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL6, EHV-1 56, EBV BBRP1, HCMV UL104, AND VZV 54.
                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                          PACKAGING.
                       222
                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
340 DSKSK 344
                                             284
                                                                     164
                                                                                          244 LSNNKELEYFVYSAPYFINNO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TaxID=57278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSV7J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 WSLPVALVALAIASIGQGVIMIVMWALEADIVEYGEYLIGVR--IEGLIYSLFSFTRKCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 IPVGFHLYSTHAALAALRGHFC--LSSDKMVCYLLKTKAIVNASEMDIQNV-----PLSE
                                                                                                                                          1 Similarity
37; Conserv
                                                             LSSDKMVCYLLKTKAI--VNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILSEVT
                                                                                                            VTNNVVLE-----APFLVGIEGSLKGSTYNLLFCGSCGIPVGFHLYSTHAALAALRGHFC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                      PDQSK 226
                                             LHRHRKMCQLLNTFPIKVLTTSKNSVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K--KFKEIVVEIDNRKKVQQQLISDIT
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                                                                                                                                                                                                                                                                                                                                                                                                               (JAN-1996)
                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GSIPAFILGLSGYIANQVQTPEVIMGIRTSIALVPCGFMLLAFVIIWFYPLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40,
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                                                                                                                                                  6.8%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 / strain JI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no RNA stage;
                                                                                                                                                                                     MW;
                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                  Score 81.5;
Pred. No. 9.
                                                                                                                                      Pred. No. 9.9;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81.5;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                    4021A6E1B453FB63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                        -KKILELIEREEKTSDAKKSLIKFLLNLS
                                                                                                                                                            DB 1;
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                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
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                                                                                                                                                                                                                                                                                                             restrictions
                                                                                                                                                            640;
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                                                                                                                                      31;
                                                                                                                                                                                                                                                                                                                           a collaboration - MBL outstation -
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                                                                                                                                                                                                                                                                                         tor
                                                                                       -ELNKHEN
                                                                                                                                                                                                                                                                                                                          outstation
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RESULT 11

chain

precursor

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RESULT 12
CA1C MOUSE S:
DT CA1C MOUSE S:
AC Q60847; P70322;
DT 15-UTL-1998 (Rel
DT 28-FEB-2003 (Rel
DT 10-OCT-2003 (Rel
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Best Local S
Matches 34
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus (type 6 / Viruses; dsDNA viruses, no l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96195263; PubMed=8634027;
Lindquester G.J., Inoue N., Allen R.D., C.
Stamey F.R., Dambaugh T.R., O'Brian J.J.,
Frenkel N., Pellett P.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Betaherpesvirinae; Roseolovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996
10-OCT-2003
                                                                                                                                                                                                                                                                                                                   3MBL; AF15,,,,
p1R; T44221.
p1R; T44221; T18002660; Herpes UL6.
InterPro; IPR002660; Herpes_UL6; 1.
pfam; PF01763; Herpes_UL6; 1.
proDom; PD003210; Herpes_UL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Restriction endonuclease mapping a
herpesvirus 6 variant B strain Z29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pellett P.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dominguez G., Dambaugh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99412318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human herpesvirus 6B genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virol. 73:8040-8052(1999).
FUNCTION: PRESUMED VIRION PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHV-1 56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSV6Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PACKAGING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human herpesvirus 6A."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virol. 141:367-379(1996)
                                                                                                                                                                                                                                   213
                                                                                                                          329
                                                                                                                                                                                                        150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein U76.
CB3L.
                                                                                                                                                                                                                                                                                        l Similarity
34; Conserv
                                                                                                                                                                                                                                   VSSKLIHDIVRHKONIVTPILLGLSSVIIPDFHNIKIFRDRNSEQISCFKNKKAIAFFTY
                                                                                                                                                                            STPYVIRNRLMLTTPLAHLSPELKKHNSLRRHQKMCQLLNTFPIKVLTAAKTDVTN
                                                                                                                                                                                                                                                             VFSRVTNNVV-----LEAPFLVGIEGSLKGSTYNL----
                                                                                                                          KKIMDMIEKEEKNSDAKKSLIKFLLNLSDSKSK 361
                                                                                                                                                                                                           STHAAL--
                                                                                                                                                   EKIAELKEKIVLTHNRLKSLMKILSEVTPDQSK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                        Conservative
    (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBV BBRF1, HCMV UL104, AND VZV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BELONGS TO FAMILY
                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10482553;
    36,
41,
42,
                                                                                                                                                                                                                                                                                                      6.8%;
    Created)
Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 / strain Z29) (HHV6).
no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                           29;
     annotation update)
               sequence
                                                                                                                                                                                                           -AALRGHFCLSSDKMVCYLLKTKAI--VNASEMDIQNVPLS 193
                                                                                                                                                                                                                                                                                                      Score 81.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stamey
                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662
                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Castelli J.W., , Danovich R.M.,
                                                                                                                                                                                                                                                                                                            10:
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                                                           ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          content and comparison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloning
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                                                                                                                                                                                                                                                                                                                        662;
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                                                                                                                                                                                                                                                                                             35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9Ta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           commercial
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Collagen alpha 1(XII)
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Boehme K., Li Y., Oh P.S., Olsen B.R.;
"Primary structure of the long and short splice variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 skin, cornea, sclera, blood vessels, and periosteum.

skin, cornea, sclera, blood vessels, and periosteum.

ENEMEDOPMENTAL STAGES The long NC3 XIIA isoforms are predominant at early stages (ED7 and 11); at later stages of development (ED15 and 17) the short NC3 XIIB forms become the major forms. As the short NC3 forms become the major product, the long splice variant continues to be expressed in several tissues, even after birth. The long NC1 isoforms, XIIA-1 and XIIB-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NC1 form XIIB-2 remains constant throughout late stages of embryonic development (ED15 and ED17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kania A.M.,
Olsen B.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     development."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen XII and their tissue-specific expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Swiss Webster, and C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural variation of type XII collagen at its cancel domain generated by tissue-specific alternative J. Biol. Chem. 274:22053-22059(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99348349;
                                                                                                                                     -!- SIMILARITY: Contains 18 fibronectin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          localized in the perifibrillar matrix (By similarity) SUBUNIT: Trimer of identical chains each containing 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            siol. Chem. 274:22053-22059(1999).

FUNCTION: Type XII collagen interacts with type I collagen-
containing fibrils, the COL1 domain could be associated with
surface of the fibrils, and the COL2 and NC3 domains may be
                                                                                                                                                           chondroitin-sulfate type (By similarity).
SIMILARITY: BELONGS TO THE THEIL ASSOCIATED INTERRUPTED HELICES (FACIT) FAMILY.
SIMILARITY: Contains 1 TSP N-terminal (TSPN)
SIMILARITY: Contains 4 VWFA domains.
                                                                                                                                                                                                                                                                                                                                             each end (By similarity).

each end (By similarity).

PTM: Prolines at the third position of the tripeptide repeating of the chains (By the chains).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=XIIA-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=4; Comment=The final tissue form of collagen XII homotrimers or any combination of the various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nontriple-helical sequences ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                           similarity).
pTM: O-glycosylation of isoform XIIA-2; glycosaminoglycan of
                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: The triple-helical tail is stabilized by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=XIIB-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=XIIA-2; Synonyms=ER#K;
SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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HSSP; P02751; IFNA.
MGD; MG1:88448; CO112a1.
InterPro; IPR008160; CO11agen.
InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003129; TSPN.
InterPro; IPR003129; TSPN.
InterPro; IPR003129; TSPN.
InterPro; IPR0021035; VWF_A.
Pfam; PP01991; CO11agen; 5.
Pfam; PP00041; fn3; 18.
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PIEROMECTIN TYPE-III 18.

VWRPA 4.

TSP N-TERMINAL.

NONHELICAL REGION (NC3).

TRIPLE-HELICAL REGION

(CC12) WITH 1 IMPERFECTION.

NONHELICAL REGION (NC2).

TRIPLE-HELICAL REGION (NC1).

TRIPLE-HELICAL REGION

(CCL1) WITH 2 IMPERFECTIONS.

NONHELICAL REGION (NC1).

CELL ATTACHMENT SITE (POTENTIAL).

HYDROXYLATION (BY SIMILARITY).

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                                                                                                                                                                                                                                                                                                                                                                                                 POLZ BAMMU STANDARD; PRT; 894 AA. Q65657; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Genome polyprotein 2 [Contains: Helper component (EC 3.4.22.45) (HC-Pro); 70 kDa protein].

Barley mild mosaic virus (strain UK-F) (BaMMV).

Viruses; ssRNA positive-strand viruses, no DNA st
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"The complete nucleotide sequence of RNA-2 of a fungally-transmitted UK isolate of barley mild mosaic bymovirus and identification of amino acid combinations possibly involved in fungus transmission.";
Virus Res. 40:149-159(1996).
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                                                                                                                                                                                                                                                                                                                                  MEDLINE=96290241; PubMed=8725111;
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                                                                    or send an email to license@isb-sib.ch).
               Pfam; PF00721;
                                        EMBL; X90904; CAA62412.1; -
                        InterPro; IPR001337;
                                                                                                                 European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                     processing of the potyviral polyprotein. SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY
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terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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                     This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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MEDLINE=94150718; PubMed=7906398;
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